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Application Serial Number: __09/674,546__

Source: __PCT09__

Date Processed by STIC: __6|6|03__

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Revised 04/24/2003

PCT09

RAW SEQUENCE LISTING   DATE: 06/06/2003
PATENT APPLICATION: US/09/674,546   TIME: 14:00:47

Input Set : E:\Chir0334.txt
Output Set: N:\CRF4\06062003\I674546.raw

```
 3 <110> APPLICANT: Fraser, Clair
 4         Galeotti, Cesira
 5         Grandi, Guido
 6         Hickey, Erin
 7         Mesignani, Vega
 8         Mora, Marirosa
 9         Peterson, Jeremy
10         Pizza, Marigrazia
11         Rappuoli, Rino
12         Ratti, Giulio
13         Scarloto, Vincenzo
14         Scarselli, Maria
15         Tettelin, Herve
16         Venter, Craig
18 <120> TITLE OF INVENTION: Neisseria Meningitidis Antigens and Compositions
20 <130> FILE REFERENCE: CHIR0334
22 <140> CURRENT APPLICATION NUMBER: 09/674,546
23 <141> CURRENT FILING DATE: 1999-04-30 (International Filing Date)
25 <160> NUMBER OF SEQ ID NOS: 3264
27 <170> SOFTWARE: PatentIn Ver. 2.1
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ERRORED SEQUENCES

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2193 <210> SEQ ID NO: 64
2194 <211> LENGTH: 234  ──────> found 202
2195 <212> TYPE: PRT
2196 <213> ORGANISM: Neisseria meningitidis
2198 <220> FEATURE:
2199 <221> NAME/KEY: UNSURE
2200 <222> LOCATION: (1)
2201 <223> OTHER INFORMATION: Xaa is any amino acid
2203 <220> FEATURE:
2204 <221> NAME/KEY: UNSURE
2205 <222> LOCATION: (34)
2206 <223> OTHER INFORMATION: Xaa is any amino acid
2208 <220> FEATURE:
2209 <221> NAME/KEY: UNSURE
2210 <222> LOCATION: (112)  ──────────────────> no Xaa found at position 112
2211 <223> OTHER INFORMATION: Xaa is any amino acid
2213 <400> SEQUENCE: 64
W--> 2214 Xaa Gln Leu Ser Lys Ser Gly Leu Asn Cys Ala Val Leu Ser Lys Val
2215  1               5                   10                  15
```

```
2217 Phe Pro Thr Arg Ser His Thr Val Ala Ala Gln Gly Gly Ile Ser Ala
2218             20              25              30
2220 Ser Xaa Gly Asn Val Gln Glu Asp Arg Trp Asp Trp His Met Tyr Asp
2221         35              40              45
2223 Thr Val Lys Gly Ser Asp Trp Leu Gly Asp Gln Asp Ala Ile Glu Phe
2224     50              55              60
2226 Met Cys Arg Ala Ala Pro Glu Ala Val Ile Glu Leu Glu His Met Gly
2227 65              70              75              80
2229 Met Pro Phe Asp Arg Val Glu Ser Gly Lys Ile Tyr Gln Arg Pro Phe
2230             85              90              95
2232 Cys Ala Val Ala Asp Arg Thr Gly His Ala Met Leu His Thr Leu Tyr
2233             100             105             110
2235 Gln Gln Asn Val Arg Ala Asn Thr Gln Phe Phe Val Glu Trp Thr Ala
2236         115             120             125
2238 Gln Asp Leu Ile Arg Asp Glu Asn Gly Asp Val Val Gly Val Thr Ala
2239     130             135             140
2241 Met Glu Met Glu Thr Gly Glu Val Tyr Ile Phe His Ala Lys Ala Val
2242 145             150             155             160
2244 Met Phe Ala Thr Gly Gly Gly Gly Arg Ile Tyr Ala Ser Ser Thr Asn
2245             165             170             175
2248 Gly Ile Pro Leu Glu Asp Met Glu Phe Trp Gln Phe Gln Pro Thr Gly
2249             180             185             190
2251 Val Ala Gly Ala Gly Val Leu Ile Thr Glu
```
E--> 2252   195   200
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3592 <210> SEQ ID NO: 98
3593 <211> LENGTH: 124
3594 <212> TYPE: PRT
3595 <213> ORGANISM: Neisseria meningitidis
3597 <400> SEQUENCE: 98
3598 Met Gln Tyr Leu Ile Val Lys Tyr Ser His Gln Ile Phe Val Thr Ile
3599 1               5               10              15
```
E--> 3601 **Thr Ile Leu Val Phe Asn Ile Arg Val Phe Xaa Leu Trp Lys Asn Pro**
```
3602             20              25              30
3604 Glu Lys Pro Leu Ala Gly Phe Trp Lys Ala Leu Pro His Leu Asn Asp
3605         35              40              45
3607 Thr Met Leu Leu Phe Thr Gly Leu Trp Leu Met Lys Ile Thr His Phe
3608     50              55              60
3610 Ser Pro Phe Asn Ala Pro Trp Leu Gly Thr Lys Ile Leu Leu Leu Leu
3611 65              70              75              80
3613 Ala Tyr Ile Ala Leu Gly Met Met Met Met Arg Ala Arg Pro Arg Ser
3614             85              90              95
3616 Thr Lys Phe Tyr Thr Val Tyr Leu Leu Ala Met Cys Cys Leu Thr Cys
3617             100             105             110
3619 Ile Val Tyr Leu Ala Lys Thr Lys Val Leu Pro Phe
3620         115             120
8134 <210> SEQ ID NO: 213
8135 <211> LENGTH: 393
8136 <212> TYPE: DNA
8137 <213> ORGANISM: Neisseria meningitidis
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[handwritten annotation:] / Xaa detected, feature required - see p. 18

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Input Set : E:\Chir0334.txt
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wrong nucleic acid designator

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 8139 <400> SEQUENCE: 213
 8140 atgggcgcgg gctggtgtcc tcccggcatc ttgggtatcg gcatcggcgg cagccgaaaa 60
 8141 agccgtgctg atggcaaaag agtccctgat gagccacatc gacattcaag aattgcagga 120
 8142 aaaggccgcg tccggcgcgg aattgtccac caccgaagcc ctgcgcctcg aactctttga 180
E--> 8143 aaaagtcaac gcgctgggoc atcggcgcac aaggcttggg cggactgacc accgtgttgg 240
E--> 8144 acgtgaaaat cctcgattat ccgacccacg ccgcctccaa accgattgcc atgattccg0 300
E--> 8145 aactgcgccg ccacccgcca cgtcgaattt gaattggacg gctcaggccc tgtcgaactc 360
E--> 8146 acgccgccgc gcgtcgaaga tggcccgatt tga                             393
 8149 <210> SEQ ID NO: 214
 8150 <211> LENGTH: 130
 8151 <212> TYPE: PRT
 8152 <213> ORGANISM: Neisseria meningitidis
 8154 <400> SEQUENCE: 214
```

— Xaa found, feature required, see p. 18

```
 8155 Met Gly Ala Gly Trp Cys Pro Pro Gly Ile Leu Gly Ile Gly Ile Gly
 8156  1               5                  10                  15
E--> 8158 Gly Xaa Ala Glu Lys Ala Val Leu Met Ala Lys Glu Ser Leu Met Ser
 8159              20                  25                  30
 8161 His Ile Asp Ile Gln Glu Leu Gln Glu Lys Ala Ala Ser Gly Ala Glu
 8162          35                  40                  45
 8164 Leu Ser Thr Thr Glu Ala Leu Arg Leu Glu Leu Phe Glu Lys Val Asn
 8165      50                  55                  60
 8167 Ala Leu Gly Ile Gly Ala Gln Gly Leu Gly Gly Leu Thr Thr Val Leu
 8168  65                  70                  75                  80
 8170 Asp Val Lys Ile Leu Asp Tyr Pro Thr His Ala Ala Ser Lys Pro Ile
 8171              85                  90                  95
 8173 Ala Met Ile Pro Asn Cys Ala Ala Thr Arg His Val Glu Phe Glu Leu
 8174              100                 105                 110
 8176 Asp Gly Ser Gly Pro Val Glu Leu Thr Pro Pro Arg Val Glu Asp Gly
 8177          115                 120                 125
 8179 Pro Ile
 8180      130
 8844 <210> SEQ ID NO: 232
 8845 <211> LENGTH: 128
 8846 <212> TYPE: PRT
 8847 <213> ORGANISM: Neisseria meningitidis
 8849 <400> SEQUENCE: 232
```

— Xaa found, same error

```
 8850 Met Cys Met Pro Tyr Lys Ile Arg Val Ser Asp Gly Ile Cys Cys Pro
 8851  1               5                  10                  15
 8853 Met Pro Ser Glu Thr Arg Asn Gln Arg Ala Ser Ala Cys Phe Lys Ser
 8854              20                  25                  30
 8856 Ser Ile Lys Ser Pro Thr Tyr Ser Lys Pro Thr Asp Arg Arg Thr Asn
 8857              35                  40                  45
 8859 Pro Gly Arg Met Leu Ala Ala Ser Phe Ser Ser Gly Cys Ile Leu Pro
 8860          50                  55                  60
 8862 Cys Val Val Val His Gly Trp Val Met Val Glu Arg Thr Ser Pro Arg
 8863  65                  70                  75                  80
 8865 Leu Ala Val Arg Glu Lys Ser Ser Thr Pro Ser Thr Thr Phe His Ala
 8866              85                  90                  95
E--> 8869 Ala Ser Xaa Ser Ala Thr Ser Lys Pro Met Thr Met Pro Pro Pro Phe
```

RAW SEQUENCE LISTING   DATE: 06/06/2003
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Input Set : E:\Chir0334.txt
Output Set: N:\CRF4\06062003\I674546.raw

```
        8870            100              105              110
E--> 8872 Cys Cys Leu Arg Ile Ser Ala Ala Xaa Gly Trp Ser Asp Asn Pro Val
     8873          115              120              125
     8894 <210> SEQ ID NO: 234
     8895 <211> LENGTH: 130
     8896 <212> TYPE: PRT
     8897 <213> ORGANISM: Neisseria meningitidis           —Some error
     8899 <400> SEQUENCE: 234
     8900 Thr Cys Met Ser Tyr Lys Ile Arg Val Ser Asp Gly Ile Cys Gly Val
     8901  1               5               10               15
E--> 8903 Phe Pro Pro Met Pro Ser Glu Xaa Arg Asn Gln Arg Ala Ser Ala Cys
     8904          20               25               30
     8906 Phe Lys Ser Ser Ile Lys Ser Pro Thr Tyr Ser Lys Pro Thr Asp Arg
     8907          35               40               45
     8909 Arg Thr Asn Pro Gly Arg Met Leu Ala Ala Ser Phe Ser Ser Gly Cys
     8910      50               55               60
     8912 Ile Leu Pro Cys Val Val Val His Gly Trp Val Met Val Glu Arg Thr
     8913  65               70               75               80
     8915 Ser Pro Arg Leu Ala Val Arg Glu Lys Ser Ser Thr Pro Ser Thr Thr
     8916          85               90               95
     8918 Phe His Ala Ala Ala Trp Ser Ala Thr Ser Lys Pro Met Thr Met Pro
     8919          100              105              110
     8921 Pro Pro Phe Cys Cys Leu Arg Ile Ser Ser Ala Gly Trp Ser Gly Asn
     8922          115              120              125
     8924 Pro Val
     8925      130
     9467 <210> SEQ ID NO: 250
     9468 <211> LENGTH: 455
     9469 <212> TYPE: PRT
     9470 <213> ORGANISM: Neisseria meningitidis           —Some error
     9472 <400> SEQUENCE: 250
     9473 Met Lys Pro Leu Asp Leu Asn Phe Ile Cys Gln Ala Leu Lys Leu Pro
     9474  1               5               10               15
     9476 Met Pro Ser Glu Ser Lys Pro Val Ser Arg Ile Val Thr Asp Ser Arg
     9477          20               25               30
     9479 Asp Ile Arg Ala Gly Asp Val Phe Phe Ala Leu Ala Gly Glu Arg Phe
     9480          35               40               45
     9482 Asp Ala His Asp Phe Val Glu Asp Val Leu Ala Ala Gly Ala Ala Ala
     9483      50               55               60
     9485 Val Val Val Ser Arg Glu Asp Cys Ala Ala Met Asp Gly Ala Leu Lys
     9486  65               70               75               80
     9488 Val Asp Asp Thr Leu Ala Ala Leu Gln Thr Leu Ala Lys Ala Trp Arg
     9489          85               90               95
     9491 Glu Asn Val Asn Pro Phe Val Phe Gly Ile Thr Gly Ser Gly Gly Lys
     9492          100              105              110
     9494 Thr Thr Val Lys Glu Met Leu Ala Ala Val Leu Arg Arg Arg Phe Gly
     9495          115              120              125
     9497 Asp Asp Ala Val Leu Ala Thr Ala Gly Asn Phe Asn Asn His Ile Gly
     9498      130              135              140
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Input Set : **E:\Chir0334.txt**
Output Set: **N:\CRF4\06062003\I674546.raw**

```
       9500 Leu Pro Leu Thr Leu Leu Lys Leu Asn Glu Lys His Arg Tyr Ala Val
       9501 145                 150                 155                 160
E-->   9503 Ile Glu Met Gly Met Asn His Phe Gly Glu Leu Ala Val Leu Thr Xaa
       9504             165                 170                 175
       9506 Ile Ala Lys Pro Asn Ala Ala Leu Val Asn Asn Ala Met Arg Ala His
       9507             180                 185                 190
       9509 Val Gly Cys Gly Phe Asp Gly Val Gly Asp Ile Ala Lys Ala Lys Ser
       9510         195                 200                 205
       9512 Glu Ile Tyr Gln Gly Leu Cys Ser Asp Gly Ile Ala Leu Ile Pro Gln
       9513     210                 215                 220
       9515 Glu Asp Ala Asn Met Ala Val Phe Lys Thr Ala Thr Leu Asn Leu Asn
       9516 225                 230                 235                 240
       9518 Thr Arg Thr Phe Gly Ile Asp Ser Gly Asp Val His Ala Glu Asn Ile
       9519             245                 250                 255
       9521 Val Leu Lys Pro Leu Ser Cys Glu Phe Asp Leu Val Cys Gly Asp Glu
       9522             260                 265                 270
       9524 Arg Ala Ala Val Val Leu Pro Val Pro Gly Arg His Asn Val His Asn
       9525         275                 280                 285
       9527 Ala Ala Ala Ala Ala Ala Leu Ala Leu Ala Ala Gly Leu Ser Leu Asn
       9528         290                 295                 300
       9530 Asp Val Ala Glu Gly Leu Lys Gly Phe Ser Asn Ile Lys Gly Arg Leu
       9531 305                 310                 315                 320
       9533 Asn Val Lys Ser Gly Ile Lys Gly Ala Thr Leu Ile Asp Asp Thr Tyr
       9534             325                 330                 335
       9536 Asn Ala Asn Pro Asp Ser Met Lys Ala Ala Ile Asp Val Leu Ala Arg
       9537             340                 345                 350
       9539 Met Pro Ala Pro Arg Ile Phe Val Met Gly Asp Met Gly Glu Leu Gly
       9540         355                 360                 365
       9542 Glu Leu Gly Glu Asp Glu Ala Ala Ala Met His Ala Glu Val Gly Ala
       9543         370                 375                 380
       9545 Tyr Ala Arg Asp Gln Gly Ile Glu Ala Ala Tyr Phe Val Gly Asp Asn
       9546 385                 390                 395                 400
       9548 Ser Val Glu Ala Ala Glu Lys Phe Gly Ala Asp Gly Leu Trp Phe Ala
       9549             405                 410                 415
       9551 Ala Lys Asp Pro Leu Ile Gln Val Leu Arg His Asp Leu Pro Glu Arg
       9552             420                 425                 430
       9554 Ala Thr Val Leu Val Lys Gly Ser Arg Phe Met Gln Met Glu Glu Val
       9555         435                 440                 445
       9557 Val Glu Ala Leu Glu Asp Lys
       9558     450                 455
       9762 <210> SEQ ID NO: 255
       9763 <211> LENGTH: 744
       9764 <212> TYPE: DNA
       9765 <213> ORGANISM: Neisseria meningitidis
       9767 <400> SEQUENCE: 255
E-->   9768 atgnngttgt tgaagttgcc tgccgtcgcc aacacggcat catcgccgaa acggcggcgc 60
       9769 aataccgcag ccagcatttc cttcaccgtc gtcttgccgc ccgaaccggt aatgccgaac 120
       9770 acaaacggat tcacattttc acgccacgcc tttgccagcg tttgcaatgc ggcaagcgtg 180
       9771 tcatcgactt tcaacgcgcc atccattgca gcacaatctt cgcgcgaaac cacaaccgcc 240
```

n found, feature required see p. 18

```
9772 gccgcaccag cagccaatac gtcttcaaca aaatcatgcg cgtcaaaccg ctcgcccgcc 300
9773 aatgcgaaaa acacatcgcc cgcgcggatg tcgcggctgt cggttacgat gcgcgacacg 360
9774 ggtttgcttt cagacggcat cggaagcttg agggcttggc agatgaaatt taggtccagt 420
9775 ggtttcatat ttactttcgt taatattcgg cggcggaca catcggtagc ggctgatttt 480
9776 tttatcgcct gttttgctgt ggtaaaacac agattatttt cccattctca ttcggsattt 540
9777 tttctgtacg tatcattttt tagacgtatt tttagtcgat ttgccttttc ccgcatacca 600
9778 cggcgcgggg tcgtcgggca gtccgtcgat aaaggcaagg ttattgcctt cgccctgcac 660
9779 atcgggaaca ttcccccaaa aatcatagcc gtcatcgggc aactcgtcgg tttcgatacc 720
9780 cgtccaactg ccgaatccgc gtaa                                        744
9783 <210> SEQ ID NO: 256
9784 <211> LENGTH: 247
9785 <212> TYPE: PRT
9786 <213> ORGANISM: Neisseria meningitidis
9788 <400> SEQUENCE: 256
```
E-->
```
9789 Met Xaa Leu Leu Lys Leu Pro Ala Val Ala Asn Thr Ala Ser Ser Pro
9790  1           5               10              15
9792 Lys Arg Arg Arg Asn Thr Ala Ala Ser Ile Ser Phe Thr Val Val Leu
9793          20              25              30
9795 Pro Pro Glu Pro Val Met Pro Asn Thr Asn Gly Phe Thr Phe Ser Arg
9796          35              40              45
9798 His Ala Phe Ala Ser Val Cys Asn Ala Ala Ser Val Ser Ser Thr Phe
9799      50              55              60
9801 Asn Ala Pro Ser Ile Ala Ala Gln Ser Ser Arg Glu Thr Thr Thr Ala
9802 65              70              75              80
9804 Ala Ala Pro Ala Ala Asn Thr Ser Ser Thr Lys Ser Cys Ala Ser Asn
9805              85              90              95
9807 Arg Ser Pro Ala Asn Ala Lys Asn Thr Ser Pro Ala Arg Met Ser Arg
9808          100             105             110
9810 Leu Ser Val Thr Met Arg Asp Thr Gly Leu Leu Ser Asp Gly Ile Gly
9811      115             120             125
9813 Ser Leu Arg Ala Trp Gln Met Lys Phe Arg Ser Ser Gly Phe Ile Phe
9814      130             135             140
9816 Thr Phe Val Asn Ile Arg Ala Ala Asp Thr Ser Val Ala Ala Asp Phe
9817 145             150             155             160
9819 Phe Ile Ala Cys Phe Ala Val Val Lys His Arg Leu Phe Ser His Ser
9820              165             170             175
```
E-->
```
9822 His Ser Xaa Phe Phe Leu Tyr Val Ser Phe Phe Arg Arg Ile Phe Ser
9823          180             185             190
9825 Arg Phe Ala Phe Ser Arg Ile Pro Arg Arg Gly Val Val Gly Gln Ser
9826      195             200             205
9828 Val Asp Lys Gly Lys Val Ile Ala Phe Ala Leu His Ile Gly Asn Ile
9829      210             215             220
9831 Pro Pro Lys Ile Ile Ala Val Ile Gly Gln Leu Val Gly Phe Asp Thr
9832 225             230             235             240
9834 Arg Pro Thr Ala Glu Ser Ala
9835             245
9987 <210> SEQ ID NO: 261
9988 <211> LENGTH: 694
9989 <212> TYPE: DNA
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```
 9990 <213> ORGANISM: Neisseria meningitidis        — n found, same error
 9992 <400> SEQUENCE: 261
 9993 atgaaacaat ccgcccgaat aaaaatatga atcagacatt actttataca ttgggcattt 60
E-->  9994 gcgcgctttt aacctttnnn nnnnnnnnnn nnnnnnnnnn nnnntatcac ccngaatatg 120
 9995 aatacggcta ccgttattct gccgtgggtg ctttggcttc ggttgtattt ttattattat 180
 9996 tggcacgcgg tttcccgcgc gtttcttcag ttgttttact gatttacgtc ggcacaaccg 240
 9997 ccctatattt gccggtcggc tggctgtatg gtgcgccgtc ttatcagata gtcggttcga 300
 9998 tattggaaag caatcctgcc gaggcgcgtg aatttgtcgg caatcttccc gggtcgcttt 360
 9999 attttgtgca ggcattattt ttcatttttg gcttgacagt ttggaaatat tgtgtatcgg 420
10000 gggggtatt tgctgacgta aaaaactata aacgccgcag caaaatatgg ctgactatat 480
10001 tattgacttt gattttgtcc tgcgcggtga tggataaaat cgccagcgat aaagatttgc 540
10002 gagaacctga tgccggcctg ttgttgaata ttttcgacct gtattacgat ttggcttccg 600
10003 cgccggcaca atatgccgcc aagcgcgccc acattttgga agcagcaaaa aaagcgtcaa 660
10004 catggcatat ccgtcatgtt gcgcccaagt ataa                              694
10007 <210> SEQ ID NO: 262
10008 <211> LENGTH: 231
10009 <212> TYPE: PRT
10010 <213> ORGANISM: Neisseria meningitidis        — Xaa — Same error
10012 <400> SEQUENCE: 262
E--> 10013 Met Lys Gln Ser Ala Arg Ile Lys Xaa Met Asn Gln Thr Leu Leu Tyr
10014  1               5                  10                  15
E--> 10016 Thr Leu Gly Ile Cys Ala Leu Leu Thr Phe Xaa Xaa Xaa Xaa Xaa Xaa
10017                 20                  25                  30
E--> 10019 Xaa Xaa Xaa Tyr His Pro Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala
10020             35                  40                  45
10022 Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly
10023         50                  55                  60
10025 Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr
10026  65                  70                  75                  80
10028 Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln
10029                 85                  90                  95
10031 Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe
10032             100                 105                 110
10034 Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe
10035             115                 120                 125
10037 Ile Phe Gly Leu Thr Val Trp Lys Tyr Cys Val Ser Gly Gly Val Phe
10038         130                 135                 140
10040 Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile
10041 145                 150                 155                 160
10043 Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Asp Lys Ile Ala Ser
10044                 165                 170                 175
10046 Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe
10047             180                 185                 190
E--> 10049 Asp Leu Tyr Tyr Asp Leu Ala Xaa Arg Ala Gly Thr Ile Cys Arg Gln
10050             195                 200                 205
10052 Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr
10053         210                 215                 220
10055 Pro Ser Cys Cys Ala Gln Val
10056 225                 230
```

```
10079 <210> SEQ ID NO: 264
10080 <211> LENGTH: 231
10081 <212> TYPE: PRT
10082 <213> ORGANISM: Neisseria meningitidis
10084 <400> SEQUENCE: 264
10085 Met Lys Gln Ser Ala Arg Ile Lys Asn Met Asp Gln Thr Leu Lys Asn
10086  1               5                  10                  15
10088 Thr Leu Gly Ile Cys Ala Leu Leu Ala Phe Cys Phe Gly Ala Ala Ile
10089             20                  25                  30
10091 Ala Ser Gly Tyr His Leu Glu Tyr Glu Tyr Gly Tyr Arg Tyr Ser Ala
10092          35                  40                  45
10094 Val Gly Ala Leu Ala Ser Val Val Phe Leu Leu Leu Leu Ala Arg Gly
10095       50                  55                  60
10097 Phe Pro Arg Val Ser Ser Val Val Leu Leu Ile Tyr Val Gly Thr Thr
10098  65                  70                  75                  80
10100 Ala Leu Tyr Leu Pro Val Gly Trp Leu Tyr Gly Ala Pro Ser Tyr Gln
10101             85                  90                  95
10103 Ile Val Gly Ser Ile Leu Glu Ser Asn Pro Ala Glu Ala Arg Glu Phe
10104          100                 105                 110
10106 Val Gly Asn Leu Pro Gly Ser Leu Tyr Phe Val Gln Ala Leu Phe Phe
10107          115                 120                 125
10109 Ile Phe Gly Leu Thr Val Trp Arg Tyr Cys Val Ser Gly Gly Val Phe
10110       130                 135                 140
10112 Ala Asp Val Lys Asn Tyr Lys Arg Arg Ser Lys Ile Trp Leu Thr Ile
10113 145                 150                 155                 160
10115 Leu Leu Thr Leu Ile Leu Ser Cys Ala Val Met Asp Lys Ile Ala Ser
10116             165                 170                 175
10118 Asp Lys Asp Leu Arg Glu Pro Asp Ala Gly Leu Leu Leu Asn Ile Phe
10119          180                 185                 190
10121 Asp Leu Tyr Tyr Asp Leu Ala Ser Xaa Ala Gly Thr Ile Cys Arg Gln
10122          195                 200                 205
10124 Ala Arg Pro His Phe Gly Ser Ser Lys Lys Ser Val Asn Met Ala Tyr
10125       210                 215                 220
10127 Pro Ser Cys Cys Ala Gln Val
10128 225                 230
10383 <210> SEQ ID NO: 274
10384 <211> LENGTH: 396
10385 <212> TYPE: PRT
10386 <213> ORGANISM: Neisseria meningitidis
10388 <400> SEQUENCE: 274
10389 Met Val Val Leu Met Thr Ala Phe Ser Leu Leu Met Ile Tyr Ser Ala
10390  1               5                  10                  15
10392 Ser Val Tyr Leu Ala Ser Lys Glu Gly Gly Asp Gln Phe Phe Tyr Leu
10393             20                  25                  30
10395 Thr Arg Gln Ala Gly Phe Val Val Ala Gly Leu Ile Ala Ser Gly Leu
10396             35                  40                  45
10398 Leu Trp Phe Leu Cys Arg Met Arg Thr Trp Arg Arg Leu Val Pro Trp
10399       50                  55                  60
10401 Ile Phe Ala Leu Ser Gly Leu Leu Leu Val Val Val Leu Ile Ala Gly
```

E--> (line 10121)

(Handwritten annotations: "Same error" appears twice; circled "Xaa" on line 10121)

RAW SEQUENCE LISTING   DATE: 06/06/2003
PATENT APPLICATION: US/09/674,546   TIME: 14:00:48

Input Set : E:\Chir0334.txt
Output Set: N:\CRF4\06062003\I674546.raw

```
10402  65                     70                  75                        80
10404  Arg Glu Ile Asn Gly Ala Thr Arg Trp Ile Pro Leu Gly Pro Leu Asn
10405                     85                  90                  95
10408  Phe Gln Pro Thr Glu Leu Phe Lys Leu Ala Val Ile Leu Tyr Leu Ala
10409                  100                 105                 110
10411  Ser Leu Phe Thr Arg Arg Glu Glu Val Leu Arg Ser Met Glu Ser Leu
10412             115                 120                 125
10414  Gly Trp Gln Ser Ile Trp Arg Gly Thr Ala Asn Leu Ile Met Ser Ala
10415        130                 135                 140
E--> 10417  Thr Asn Pro Gln Xaa Arg Arg Glu Thr Leu Glu Met Tyr Gly Arg Xaa
10418  145                 150                 155                 160
10420  Arg Ala Ile Ile Leu Pro Ile Met Leu Val Ala Phe Gly Leu Val Leu
10421             165                 170                 175
10423  Ile Met Val Gln Pro Asp Phe Gly Ser Phe Val Val Ile Thr Val Ile
10424             180                 185                 190
10426  Ala Val Gly Met Leu Phe Leu Ala Gly Leu Pro Trp Lys Tyr Phe Phe
10427        195                 200                 205
10429  Val Leu Val Gly Ser Val Leu Gly Gly Met Val Leu Met Ile Thr Ala
10430     210                 215                 220
10432  Ala Pro Tyr Arg Val Gln Arg Val Val Ala Phe Leu Asp Pro Trp Lys
10433  225                 230                 235                 240
10435  Asp Pro Gln Gly Ala Gly Tyr Gln Leu Thr His Ser Leu Met Ala Ile
10436             245                 250                 255
10438  Gly Arg Gly Glu Trp Phe Gly Met Gly Leu Gly Ala Ser Leu Ser Lys
10439             260                 265                 270
10441  Arg Gly Phe Leu Pro Glu Ala His Thr Asp Phe Ile Phe Ala Ile Ile
10442        275                 280                 285
10444  Ala Glu Glu Phe Gly Phe Phe Gly Met Cys Val Leu Ile Phe Cys Tyr
10445     290                 295                 300
10447  Gly Trp Leu Val Val Arg Ala Phe Ser Ile Gly Lys Gln Ser Arg Asp
10448  305                 310                 315                 320
10450  Leu Gly Leu Thr Phe Asn Ala Tyr Ile Ala Ser Gly Ile Gly Ile Trp
10451             325                 330                 335
E--> 10453  Ile Gly Xaa Gln Ser Phe Phe Asn Ile Gly Val Asn Ile Gly Ala Leu
10454             340                 345                 350
E--> 10456  Pro Xaa Lys Gly Leu Thr Xaa Pro Xaa Met Ser Xaa Gly Gly Ser Ser
10457        355                 360                 365
E--> 10459  Val Phe Phe Met Leu Ile Ser Met Met Leu Leu Xaa Arg Ile Asp Tyr
10460     370                 375                 380
10462  Glu Asn Arg Arg Lys Met Arg Gly Tyr Arg Val Glu
10463  385                 390                 395
10678  <210> SEQ ID NO: 279
10679  <211> LENGTH: 1008
10680  <212> TYPE: DNA
10681  <213> ORGANISM: Neisseria meningitidis
10683  <400> SEQUENCE: 279
10684  atgggcggta aaacctttat gctgawkkcg ggcggaacgg gcggacatat tttccccgcg   60
10685  ctggcggtgg cggattcatt gcgcgcgcgc ggccatcatg tgatttggct gggcagcaag  120
10686  gattcgatgg aagagcgtat cgtgccgcaa tacggcatac gcttggaaac gctggcgatt  180
```

— *some err* (handwritten annotation)

```
      10687 aaaggcgtgc gcggcaacgg catcaaacgc aaactgatgc tgccggttac tttgtatcaa 240
      10688 accgtccgcg aagcgcagcg gattatccgc aaacaccgtg tcgagtgcgt catcggcttc 300
      10689 ggcggcttcg ttaccttccc cggcggtttg gcggcgaagc tattargcgt gccgattgtg 360
      10690 attcacgagc aaaacgccgt ggcaggtttg tccaaccgcc acctgtcgcg ctgggcgaag 420
      10691 cgggtgttgt acgcttttcc gaaagcgttc agccacgaag gcggcttggt cggcaacccc 480
      10692 gtccgcgccg atattagcaa cctgcccgtg cctgccgaac gcttccaagg gcgtgaaggc 540
      10693 cgtctgaaaa ttttggtggt cggcggcagt ttgggcgcgg acgttttgaa caaaaccgta 600
      10694 ccgcatgcat tggctttgct gcccgacaat gcgcgtccgc atatgtacca ccaatcggga 660
E--> 10695 cggggcaagc tgggcatctt gcaggcgnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 720
E--> 10696 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnngcgggat tgggtgcgtt gttagtgccg 780
      10697 tatcctcacg cggttgacga tcaccaaacc gccaacgcgc gttttatggt gcaggcggag 840
      10698 gcgggattgc tgttgccgca aacccagttg acggcggaaa aactcgccga gattctcggc 900
      10699 ggcttaaacc gcgaaaaatg cctcaaatgg gcagaaacg cccgtacgtt ggcactgccg 960
      10700 cacagtgcgg acgacgtggc ggaagccgcg attgcgtgtg cggcgtaa             1008
      10703 <210> SEQ ID NO: 280
      10704 <211> LENGTH: 335
      10705 <212> TYPE: PRT
      10706 <213> ORGANISM: Neisseria meningitidis           — Some erro
      10708 <400> SEQUENCE: 280
E--> 10709 Met Gly Gly Lys Thr Phe Met Leu Xaa Xaa Gly Gly Thr Gly Gly His
      10710  1               5                  10                  15
      10712 Ile Phe Pro Ala Leu Ala Val Ala Asp Ser Leu Arg Ala Arg Gly His
      10713              20                  25                  30
      10715 His Val Ile Trp Leu Gly Ser Lys Asp Ser Met Glu Glu Arg Ile Val
      10716              35                  40                  45
      10718 Pro Gln Tyr Gly Ile Arg Leu Glu Thr Leu Ala Ile Lys Gly Val Arg
      10719          50                  55                  60
      10721 Gly Asn Gly Ile Lys Arg Lys Leu Met Leu Pro Val Thr Leu Tyr Gln
      10722 65                  70                  75                  80
      10724 Thr Val Arg Glu Ala Gln Arg Ile Ile Arg Lys His Arg Val Glu Cys
      10725              85                  90                  95
      10727 Val Ile Gly Phe Gly Gly Phe Val Thr Phe Pro Gly Gly Leu Ala Ala
      10728              100                 105                 110
E--> 10730 Lys Leu Leu Xaa Val Pro Ile Val Ile His Glu Gln Asn Ala Val Ala
      10731          115                 120                 125
      10733 Gly Leu Ser Asn Arg His Leu Ser Arg Trp Ala Lys Arg Val Leu Tyr
      10734          130                 135                 140
      10736 Ala Phe Pro Lys Ala Phe Ser His Glu Gly Gly Leu Val Gly Asn Pro
      10737 145                 150                 155                 160
      10739 Val Arg Ala Asp Ile Ser Asn Leu Pro Val Pro Ala Glu Arg Phe Gln
      10740              165                 170                 175
      10742 Gly Arg Glu Gly Arg Leu Lys Ile Leu Val Val Gly Gly Ser Leu Gly
      10743              180                 185                 190
      10745 Ala Asp Val Leu Asn Lys Thr Val Pro His Ala Leu Ala Leu Leu Pro
      10746          195                 200                 205
      10748 Asp Asn Ala Arg Pro His Met Tyr His Gln Ser Gly Arg Gly Lys Leu
      10749          210                 215                 220
E--> 10751 Gly Ile Leu Gln Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      10752 225                 230                 235                 240
```

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        Input Set : E:\Chir0334.txt
        Output Set: N:\CRF4\06062003\I674546.raw

```
E--> 10754 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Gly Leu Gly Ala
     10755                 245                 250                 255
     10757 Leu Leu Val Pro Tyr Pro His Ala Val Asp Asp His Gln Thr Ala Asn
     10758             260                 265                 270
     10760 Ala Arg Phe Met Val Gln Ala Glu Ala Gly Leu Leu Leu Pro Gln Thr
     10761         275                 280                 285
     10763 Gln Leu Thr Ala Glu Lys Leu Ala Glu Ile Leu Gly Gly Leu Asn Arg
     10764     290                 295                 300
     10766 Glu Lys Cys Leu Lys Trp Ala Glu Asn Ala Arg Thr Leu Ala Leu Pro
     10767 305                 310                 315                 320
     10769 His Ser Ala Asp Asp Val Ala Glu Ala Ala Ile Ala Cys Ala Ala
     10770             325                 330                 335
     10982 <210> SEQ ID NO: 285
     10983 <211> LENGTH: 1131
     10984 <212> TYPE: DNA
     10985 <213> ORGANISM: Neisseria meningitidis          —Some error
     10987 <400> SEQUENCE: 285
E--> 10988 atgtttttat ggctcgcaca tttcagcanc tggttaaccg gtctgaatnn nnnnnnnnnn 60
E--> 10989 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
E--> 10990 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180
E--> 10991 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 240
E--> 10992 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 300
E--> 10993 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
E--> 10994 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 420
E--> 10995 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 480
E--> 10996 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnggcgtgg tcggcttttt ggtgttgtct 540
     10997 tacctgacca tcgtcggcac atccaatgcc gtcaacctca ccgacggctt ggacggcctt 600
     10998 gcgaccttcc ccgtcgtcct cgttgccgcc ggcctcgcca tcttcgccta tgccagcggc 660
     10999 cactcacaat ttgcccaata cctgcaatta ccttacgttg ccggcgcaaa cgaagtggtg 720
     11000 attttctgta ccgccatgtg cggcgcgtgc ctcggttttct tgtggtttaa cgcctatccc 780
     11001 gcgcaagtct ttatgggcga tgtcggtgca ttggcattgg gtgccgcgct cggtaccgtc 840
     11002 gccgttatcg tccgccaaga gtttgtcctc gtcattatgg gcggattatt tgtcgtagaa 900
     11003 gccgtatccg ttatgcttca ggttggctgg tataagaaaa ccaaaaaacg catcttcctg 960
     11004 atggcgccca tccatcacca ctacgaacaa aaaggctgga agaaaccca agtcgtcgtc 1020
     11005 cgcttttgga ttattaccat cgtcttggtg ttgatcggtt tgagtaccct caaaatccgc 1080
     11006 tgaacctatg ccgtctgaac atctttcaga cggcatttga acgcgcaata a         1131
     11009 <210> SEQ ID NO: 286
     11010 <211> LENGTH: 376
     11011 <212> TYPE: PRT
     11012 <213> ORGANISM: Neisseria meningitidis
     11014 <400> SEQUENCE: 286
     11015 Met Phe Leu Trp Leu Ala His Phe Ser Asn Trp Leu Thr Gly Leu Asn
     11016   1                 5                  10                  15
     11018 Ile Phe Gln Tyr Thr Thr Phe Arg Ala Val Met Ala Ala Leu Thr Ala
     11019             20                  25                  30
     11021 Leu Ala Phe Ser Leu Met Phe Gly Pro Trp Thr Ile Arg Arg Leu Thr
     11022         35                  40                  45
     11024 Ala Leu Lys Cys Gly Gln Ala Val Arg Thr Asp Gly Pro Gln Thr His
     11025         ·50                 55                  60
```

```
11027 Leu Val Lys Asn Gly Thr Pro Thr Met Gly Gly Ser Leu Ile Leu Thr
11028  65               70               75               80
11030 Ala Ile Thr Val Ser Thr Leu Leu Trp Gly Asn Trp Ala Asn Pro Tyr
11031              85               90               95
11033 Ile Trp Ile Leu Leu Gly Val Leu Leu Ala Thr Gly Ala Leu Gly Phe
11034             100              105              110
11036 Tyr Asp Asp Trp Arg Lys Val Val Tyr Lys Asp Pro Asn Gly Val Ser
11037         115              120              125
11039 Ala Lys Phe Lys Met Val Trp Gln Ser Ser Val Ala Val Ile Ala Gly
11040     130              135              140
11042 Leu Ala Leu Phe Tyr Leu Ala Ala Asn Ser Ala Asn Asn Ile Leu Ile
11043 145              150              155              160
11045 Val Pro Phe Phe Lys Gln Ile Ala Leu Pro Leu Gly Val Val Gly Phe
11046             165              170              175
11048 Leu Val Leu Ser Tyr Leu Thr Ile Val Gly Thr Ser Asn Ala Val Asn
11049             180              185              190
11051 Leu Thr Asp Gly Leu Asp Gly Leu Ala Thr Phe Pro Val Val Leu Val
11052         195              200              205
11054 Ala Ala Gly Leu Ala Ile Phe Ala Tyr Ala Ser Gly His Ser Gln Phe
11055     210              215              220
11057 Ala Gln Tyr Leu Gln Leu Pro Tyr Val Ala Gly Ala Asn Glu Val Val
11058 225              230              235              240
11060 Ile Phe Cys Thr Ala Met Cys Gly Ala Cys Leu Gly Phe Leu Trp Phe
11061             245              250              255
11063 Asn Ala Tyr Pro Ala Gln Val Phe Met Gly Asp Val Gly Ala Leu Ala
11064             260              265              270
11066 Leu Gly Ala Ala Leu Gly Thr Val Ala Val Ile Val Arg Gln Glu Phe
11067     275              280              285
11069 Val Leu Val Ile Met Gly Gly Leu Phe Val Val Glu Ala Val Ser Val
11070     290              295              300
11072 Met Leu Gln Val Gly Trp Tyr Lys Lys Thr Lys Lys Arg Ile Phe Leu
11073 305              310              315              320
11075 Met Ala Pro Ile His His His Tyr Glu Gln Lys Gly Trp Lys Glu Thr
11076             325              330              335
11078 Gln Val Val Val Arg Phe Trp Ile Ile Thr Ile Val Leu Val Leu Ile
11079             340              345              350
```

E--> **11081 Gly Leu Ser Thr Leu Lys Ile Arg Xaa Thr Tyr Ala Val Xaa Thr Ser**
```
11082         355              360              365
11084 Phe Arg Arg His Leu Asn Ala Gln
11085     370              375
11263 <210> SEQ ID NO: 292
11264 <211> LENGTH: 149
11265 <212> TYPE: PRT
11266 <213> ORGANISM: Neisseria meningitidis
11268 <400> SEQUENCE: 292
```

~ Some err

E--> **11269 Met Pro Pro Lys Ile Thr Xaa Ser Gly Phe Cys Lys Pro Ala Ile Ala**
```
11270   1           5               10              15
11272 Ala Ala Val Ala Pro Thr Phe Val Pro Leu Leu Ser Ser Ile Asn Thr
11273             20              25              30
```

RAW SEQUENCE LISTING   DATE: 06/06/2003
PATENT APPLICATION: US/09/674,546   TIME: 14:00:48

Input Set : E:\Chir0334.txt
Output Set: N:\CRF4\06062003\I674546.raw

```
11275 Thr Pro Phe Phe Ser Pro Ile Phe Ser Thr Arg Cys Gly Arg Pro Trp
11276         35                40                45
11278 Lys Val Leu Thr Cys Ser Ser Asn Ala Ser Arg Asp Lys Pro Met Ala
11279         50                55                60
E--> 11281 Ser His Lys Ala Thr Ala Ala Met Thr Leu Ala Ala Leu Cys Xaa Pro
11282 65                70                75                80
11284 Cys Asn Gly Met Ser Cys Val Thr Ile Lys Ser Ser Leu Pro Cys Phe
11285             85                90                95
11287 Arg Arg Pro Val Ser Arg Ser Asn Gln Lys Ser Ala Ser Cys Ser Asn
11288             100               105               110
11290 Glu Asn His Phe Thr Ser Arg Pro Ala Arg Phe Ile Ala Arg Gln Asn
11291         115               120               125
11293 Ala Ser Ser Ala Phe Lys Thr Cys Thr Pro Ser Pro Arg Lys Ile Leu
11294         130               135               140
11296 Ala Leu Val Cys Ala
11297 145
11367 <210> SEQ ID NO: 296
11368 <211> LENGTH: 118
11369 <212> TYPE: PRT
11370 <213> ORGANISM: Neisseria gonorrhoeae
11372 <400> SEQUENCE: 296
11373 Met Arg Val Val Glu Gln Ile Val Val Ala Val Glu Met Val Phe Gly
11374 1               5                 10                15
11376 Asn Val His His Arg Arg Arg Ser Arg Ala Gln Ala Phe Gly Val Phe
11377             20                25                30
11379 Gln Leu Glu Ala Gly Lys Leu Pro His Pro His Val Arg Leu Phe Ala
11380         35                40                45
11382 Phe Ala Leu Gln Phe Cys Leu Gln Asp Gly Arg Thr Asp Ile Ala Arg
11383         50                55                60
11385 Asn Asp Gly Ile Gln Pro Ala Leu Asp Ala Glu Ile Ala Asp Gln Ala
11386 65                70                75                80
11388 Gly Tyr Arg Gly Phe Ala Val Ala Ala Gly Asn Arg Asn His Leu Val
11389             85                90                95
E--> 11391 Ala Ala Ala Val His Asn Val Arg Gln Gln Leu Asp Val Ala Xaa His
11392             100               105               110
E--> 11394 Ala Xaa Arg Arg Phe Ala
11395         115
11412 <210> SEQ ID NO: 298
11413 <211> LENGTH: 118
11414 <212> TYPE: PRT
11415 <213> ORGANISM: Neisseria meningitidis
11417 <400> SEQUENCE: 298
11418 Met Arg Ile Val Glu Gln Val Val Val Ala Val Glu Met Val Phe Gly
11419 1               5                 10                15
11421 Asn Val Gln His Arg Arg Arg Ser Arg Thr Gln Ala Phe Gly Val Phe
11422             20                25                30
11424 Gln Leu Glu Ala Gly Lys Leu Gln His Pro His Val Arg Leu Phe Ala
11425         35                40                45
11427 Phe Ala Leu Pro Phe Arg Leu Gln Asn Arg Arg Ala Asp Ile Ala Arg
```

— Same error

— Same error

```
11428       50                    55                    60
11430 Asp Asn Gly Ile Gln Pro Ala Leu Asp Thr Glu Ile Ala Asp Gln Ala
11431  65                   70                    75                    80
11433 Arg Tyr Arg Gly Phe Ala Val Ala Ala Gly Asn Arg Asn Tyr Leu Val
11434                   85                    90                    95
11436 Val Pro Ala Val His Asn Val Arg Gln Gln Phe Asp Val Ala Gln His
11437              100                   105                   110
E-->  11439 Ala Xaa Arg Arg Phe Ala
11440         115
11457 <210> SEQ ID NO: 300
11458 <211> LENGTH: 118
11459 <212> TYPE: PRT
11460 <213> ORGANISM: Neisseria meningitidis
11462 <400> SEQUENCE: 300
11463 Met Arg Val Val Glu Gln Val Val Val Ala Val Glu Met Val Phe Gly
11464   1                   5                    10                    15
11466 Asn Val Gln His Cys Arg Arg Ser Arg Ala Gln Ala Phe Gly Val Phe
11467                   20                    25                    30
11469 Gln Leu Glu Thr Gly Lys Leu Gln His Pro His Val Arg Leu Phe Ala
11470              35                    40                    45
11472 Phe Ala Leu Gln Phe Arg Leu Gln Asn Arg Arg Ala Asp Ile Ala Arg
11473       50                    55                    60
11475 Asp Asn Gly Ile Gln Pro Thr Leu Asp Ala Glu Ile Ala Asp Gln Ala
11476  65                   70                    75                    80
11478 Arg Tyr Arg Gly Phe Ala Val Ala Ala Gly Asn Arg Asn His Leu Val
11479                   85                    90                    95
11481 Ala Ala Ala Val His Asn Val Arg Gln Gln Phe Asp Val Ala Gln His
11482              100                   105                   110
E-->  11484 Ala Xaa Arg Arg Phe Ala
11485         115
12254 <210> SEQ ID NO: 318
12255 <211> LENGTH: 276
12256 <212> TYPE: PRT
12257 <213> ORGANISM: Neisseria meningitidis
12259 <400> SEQUENCE: 318
12260 Met Gln Asn Phe Gly Lys Val Ala Val Leu Met Gly Gly Phe Ser Ser
12261   1                   5                    10                    15
12263 Glu Arg Glu Ile Ser Leu Asp Ser Gly Thr Ala Ile Leu Asn Ala Leu
12264                   20                    25                    30
12266 Lys Ser Lys Gly Ile Asp Ala Tyr Ala Phe Asp Pro Lys Glu Thr Pro
12267              35                    40                    45
12269 Leu Ser Glu Leu Lys Ala Gln Gly Phe Gln Thr Ala Phe Asn Ile Leu
12270       50                    55                    60
E-->  12272 His Gly Thr Tyr Gly Xaa Asp Gly Ala Val Gln Gly Ala Leu Glu Leu
12273  65                   70                    75                    80
12275 Leu Gly Ile Pro Tyr Thr Gly Ser Gly Val Ala Ala Ser Ala Ile Gly
12276                   85                    90                    95
12278 Met Asp Lys Tyr Arg Cys Lys Leu Ile Trp Gln Ala Leu Gly Leu Pro
12279              100                   105                   110
```

RAW SEQUENCE LISTING   DATE: 06/06/2003
PATENT APPLICATION: US/09/674,546   TIME: 14:00:48

Input Set : E:\Chir0334.txt
Output Set: N:\CRF4\06062003\I674546.raw

```
  12281 Val Pro Glu Phe Ala Val Leu His Asp Asp Thr Asp Phe Asp Ala Val
  12282         115                 120             125
  12284 Glu Glu Lys Leu Gly Leu Pro Met Phe Val Lys Pro Ala Ala Glu Gly
  12285         130                 135             140
  12287 Ser Ser Val Gly Val Val Lys Val Lys Gly Lys Gly Arg Leu Lys Ser
  12288 145                 150             155                 160
E--> 12290 Val Tyr Glu Glu Leu Lys His Leu Gln Xaa Arg Asn His Cys Arg Thr
  12291             165                 170             175
  12293 Phe Tyr Arg Arg Arg Arg Ile Phe Leu Pro Arg Pro Glu Arg Gln Arg
  12294         180                 185             190
  12296 Ala Ala Arg His Thr His His Ser Arg Asn Arg Val Leu Arg Leu Arg
  12297         195                 200             205
  12299 Ser Gln Val Gln Pro Arg Arg His His Leu Ser Met Ser Phe Gly Arg
  12300         210                 215             220
  12302 Phe Asp Arg Ser Arg Arg Lys Pro Asp Ala Arg Thr Gly Gly Ser Arg
  12303 225                 230             235                 240
  12305 Arg Ala Gly Asn Arg Cys Gly Arg Leu Arg Ala Arg Arg Phe Pro Gln
  12306             245                 250             255
  12308 Arg Tyr Arg Arg Gln Thr Leu Ser Val Gly Asn Gln His Pro Ala Arg
  12309             260                 265             270
  12311 Tyr Asp Glu Pro
  12312         275
  76670 <210> SEQ ID NO: 1818
  76671 <211> LENGTH: 770
  76672 <212> TYPE: PRT
  76673 <213> ORGANISM: Neisseria meningitidis
  76675 <400> SEQUENCE: 1818
  76676 Gly Asx Asx Phe Phe Phe Phe Phe Leu Phe Ala Leu Met Lys Arg Ile
  76677   1             5                 10                  15
  76679 Phe Leu Pro Ala Leu Pro Ala Ile Leu Pro Leu Ser Thr Tyr Ala Asp
  76680             20                 25                  30
  76682 Leu Pro Leu Thr Ile Glu Asp Ile Met Thr Asp Lys Gly Lys Trp Lys
  76683         35                 40                  45
  76685 Leu Glu Thr Ser Leu Thr Tyr Leu Asn Ser Glu Asn Asn Arg Ala Glu
  76686         50                 55                  60
  76688 Leu Ala Ala Pro Val Tyr Ile Gln Thr Gly Ala Thr Ser Phe Ile Pro
  76689 65                 70                 75                  80
  76691 Ile Pro Thr Glu Ile Gln Glu Asn Gly Ser Asn Thr Asp Met Leu Val
  76692             85                 90                  95
  76694 Gly Thr Leu Gly Leu Arg Tyr Gly Leu Thr Gly Asn Thr Asp Ile Tyr
  76695         100                 105                110
  76697 Gly Ser Gly Ser Tyr Leu Trp His Glu Glu Arg Lys Leu Asp Gly Asn
  76698         115                 120                125
  76700 Ser Lys Thr Arg Asn Lys Arg Met Ser Asp Val Ser Leu Gly Ile Ser
  76701         130                 135                140
  76703 His Thr Phe Leu Lys Asp Asp Lys Asn Pro Ala Leu Ile Ser Phe Leu
  76704 145                 150                155                 160
  76706 Glu Ser Thr Val Tyr Glu Lys Ser Arg Asn Lys Ala Ser Ser Gly Lys
  76707             165                 170                175
```

Handwritten annotations: "found 722!" (with arrow from LENGTH: 770), "—some error"

```
       76709 Ser Trp Leu Ile Gly Ala Thr Thr Tyr Lys Ala Ile Asp Pro Ile Val
       76710             180                 185                 190
       76712 Leu Ser Leu Thr Ala Ala Tyr Arg Ile Asn Gly Ser Lys Thr Leu Ser
       76713             195                 200                 205
       76715 Asp Gly Ile Arg Tyr Lys Ser Gly Asn Tyr Leu Leu Leu Asn Pro Asn
       76716       210                 215                 220
       76718 Ile Ser Phe Ala Ala Asn Asp Arg Ile Ser Leu Thr Gly Gly Ile Gln
       76719 225                 230                 235                 240
       76721 Trp Leu Gly Arg Gln Pro Asp Arg Thr Asp Gly Lys Arg Glu Ser Ser
       76722             245                 250                 255
       76724 Arg Asn Thr Ser Thr Tyr Ala His Phe Gly Ala Gly Phe Gly Phe Thr
       76725             260                 265                 270
       76727 Lys Thr Thr Ala Leu Asn Ala Ser Ala Arg Phe Asn Val Ser Gly Gln
       76728             275                 280                 285
       76730 Cys Tyr Glx Asn Arg Met Ala Leu Met His Ala Asp Glu Phe Ala Leu
       76731       290                 295                 300
       76733 Thr Pro Ala Arg Ala Gly Arg Ala Pro His Phe Asn Thr Asp Asp Ser
       76734 305                 310                 315                 320
       76736 Glu Gln Glu Asn Cys Glu Cys Gln His Met His Asn His Ala His Trp
       76737             325                 330                 335
       76739 His Lys Ser Glu Arg Val Glu Arg Asp Ala Thr Ala Met His Cys His
       76740             340                 345                 350
       76742 Ile Arg Asn Asx Ser Glu Asp Cys Glx Glx Glx Pro Gly Thr Ile
       76743             355                 360                 365
       76745 Met Glu Ser Asn Glu Trp Arg Met Ala Asn Ser Tyr Met Asx Leu Ala
       76746       370                 375                 380
       76748 Arg Ile Ala Leu Cys Arg Ile Glu Arg Asn Glu Trp His Cys Phe Cys
       76749 385                 390                 395                 400
       76751 Phe Met Lys Arg Ile Phe Leu Pro Ala Leu Pro Ala Ile Leu Pro Leu
       76752             405                 410                 415
       76754 Ser Thr Tyr Ala Asp Leu Pro Leu Thr Ile Glu Asp Ile Met Thr Asp
       76755             420                 425                 430
       76757 Lys Gly Lys Trp Lys Leu Glu Thr Ser Leu Thr Tyr Leu Asn Ser Glu
       76758             435                 440                 445
E-->   76760 Asn Asn Arg His Lys His Lys His Asp Pro His Pro Xaa Met Lys Arg
       76761       450                 455                 460
       76763 Ile Phe Leu Pro Ala Leu Pro Ala Ile Leu Pro Leu Ser Thr Tyr Ala
       76764 465                 470                 475                 480
       76766 Asp Leu Pro Leu Thr Ile Glu Asp Ile Met Thr Asp Lys Gly Lys Trp
       76767             485                 490                 495
       76769 Lys Leu Glu Thr Ser Leu Thr Tyr Leu Asn Ser Glu Asn Asn Arg Met
       76770             500                 505                 510
       76772 His Lys Arg Ile Phe His Lys Asn Arg Met Ala Leu Phe His Lys Leu
       76773             515                 520                 525
       76775 Phe Lys Met Ile Cys Arg Ser Phe Thr Trp Arg Asp Ser Ala Ala Asp
       76776       530                 535                 540
       76778 Leu His Pro Trp Trp Lys Met Asn Phe Met Lys Arg Ile Phe Leu Pro
       76779 545                 550                 555                 560
       76781 Ala Leu Pro Ala Ile Leu Pro Leu Ser Thr Tyr Ala Asp Leu Pro Leu
```

```
76782                   565                 570                     575
76784 Thr Ile Glu Asp Ile Met Thr Asp Lys Gly Lys Trp Lys Leu Glu Thr
76785               580                 585                 590
76787 Ser Leu Thr Tyr Leu Asn Ser Glu Asn Asn Arg Thr Ile Thr Leu Glu
76788           595                 600                 605
76790 Pro Ile Asp Gly Ile Asp Ala Asn Glu Ala Asp Asp Ala Glu Ala Cys
76791       610                 615                 620
76793 Asx Asp Cys Arg Thr Glu Asn Thr Arg Tyr Arg Glu Phe His Tyr Ala
76794 625                 630                 635                     640
76796 Pro Ala Thr Ala Asx Leu Glu Trp Arg Asp Asp Cys Met Glu Asn Thr
76797               645                 650                 655
76799 Ser Met Met Ala Arg Tyr Ile Asn Phe Arg Met Ala Thr Ile Asn Asp
76800               660                 665                 670
76802 Cys Met Glu Asn Thr Ser Met Met Ala Arg Tyr Ile Asn Phe Arg Met
76803           675                 680                 685
76805 Phe Met Ile Cys Arg Ser Phe Thr Trp Arg Asp Asp Cys Met Glu Asn
76806       690                 695                 700
76808 Thr Met Ser Trp Arg Asp Asp Cys Trp Arg Asp Asp Cys Met Glu Asn
76809 705                 710                 715                     720
E--> 76811 Thr Gln
```

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Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:4; Xaa Pos. 19,21,24
Seq#:7; N Pos. 529
Seq#:10; Xaa Pos. 19,59,107,114,208
Seq#:21; N Pos. 350,374,375,376,377,378,379,380,381,382,383,384,385,386,387
Seq#:21; N Pos. 388,389,390,391,392,393,394,395,396,397,398,399,400,401,402
Seq#:21; N Pos. 403,404,405,406,407,408,409,410,411,412,413,414,415,416,417
Seq#:21; N Pos. 418,419,420,421,422,423,424,425,426,427,428,429,430,431,432
Seq#:21; N Pos. 433,434,435,436,437,438,439,440,441,442,443,444,445,446,447
Seq#:21; N Pos. 448,449,450,451,452,453,454,455,456,457,458,459,460,461,462
Seq#:21; N Pos. 463,464,465,466,467,468,469,470,471,472,473,474,475,476,477
Seq#:21; N Pos. 478,479,480,481,482,483,484,485,486,487,488,489,490,491,492
Seq#:21; N Pos. 493,494,495,496,497,498,499,500,501,502,503,504,505,506,507
Seq#:21; N Pos. 508,509,510,511,512,513,514,515,516,517,518,519,520,521,522
Seq#:21; N Pos. 523,524,525,526,527,528,529,530,531,532,533,534,535,536,537
Seq#:21; N Pos. 538,539,540,541,542,543,544,545,546,547,548,549,550,551,552
Seq#:21; N Pos. 553,554,555,556,557,558,559,560,561,562,563,564,565,566,567
Seq#:21; N Pos. 568,569,570,571,572,573,574,575,576,577,578,579,580,581
Seq#:22; Xaa Pos. 54,104,117,125,126,127,128,129,130,131,132,133,134,135
Seq#:22; Xaa Pos. 136,137,138,139,140,141,142,143,144,145,146,147,148,149
Seq#:22; Xaa Pos. 150,151,152,153,154,155,156,157,158,159,160,161,162,163
Seq#:22; Xaa Pos. 164,165,166,167,168,169,170,171,172,173,174,175,176,177
Seq#:22; Xaa Pos. 178,179,180,181,182,183,184,185,186,187,188,189,190,191
Seq#:22; Xaa Pos. 192,193,194
Seq#:40; Xaa Pos. 84
Seq#:52; Xaa Pos. 98
Seq#:63; N Pos. 1,100
Seq#:64; Xaa Pos. 1,34
Seq#:65; N Pos. 67,408
Seq#:66; Xaa Pos. 23
Seq#:71; N Pos. 67,408
Seq#:72; Xaa Pos. 23
Seq#:79; N Pos. 310,311,312,313,314,315,316,317,318,319,320,321,322,323,324
Seq#:79; N Pos. 325,326,327,328,329,330,331,332,333,334,335,336,337,338,339
Seq#:79; N Pos. 340,341,342,343,344,345,346,347,348,349,350,351,352,353,354
Seq#:79; N Pos. 355,356,357,358,359,360,361,362,363,364,365,366,367,368,369
Seq#:79; N Pos. 370,371,372,373,374,375,376,377,378,379,380,381,382,383,384
Seq#:79; N Pos. 385,386,387,388,389,390,391,392,393,394,395,396,397,398,399
Seq#:79; N Pos. 400,401,402,403,404,405,406,407,408,409,410,411,412,413,414
Seq#:79; N Pos. 415,416,417,418,419,420,421,422,423,424,425,426,427,428,429
Seq#:79; N Pos. 430,431,432,433,434,435,436,437,438,439,440,441,442,443,444
Seq#:79; N Pos. 445,446,447,448,449,450,451,452,453,454,455,456,457,458,459
Seq#:79; N Pos. 460,461,462,463,464,465,466,467,468,469,470,471,472,473,474
Seq#:79; N Pos. 475,476,477,478,479,480,481,482,483,484,485,486,487,488,489

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```
Seq#:79; N Pos.  490,491,492,493,494,495,496,497,498,499,500,501,502,503,504
Seq#:79; N Pos.  505,506,507,508,509,510,511,512,513,514,515,516,517,518,519
Seq#:79; N Pos.  541
Seq#:80; Xaa Pos. 104,105,106,107,108,109,110,111,112,113,114,115,116,117
Seq#:80; Xaa Pos. 118,119,120,121,122,123,124,125,126,127,128,129,130,131
Seq#:80; Xaa Pos. 132,133,134,135,136,137,138,139,140,141,142,143,144,145
Seq#:80; Xaa Pos. 146,147,148,149,150,151,152,153,154,155,156,157,158,159
Seq#:80; Xaa Pos. 160,161,162,163,164,165,166,167,168,169,170,171,172,173
```

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Input Set : **E:\Chir0334.txt**
Output Set: **N:\CRF4\06062003\I674546.raw**

L:23 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD
L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:16
L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:480
L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:16
M:341 Repeated in SeqNo=10
L:792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:300
M:341 Repeated in SeqNo=21
L:843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:48
M:341 Repeated in SeqNo=22
L:1513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:80
L:1862 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:96
L:2179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63 after pos.:0
M:341 Repeated in SeqNo=63
L:2214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64 after pos.:0
M:341 Repeated in SeqNo=64
L:2252 M:252 E: No. of Seq. differs, <211> LENGTH:Input:234 Found:202 SEQ:64
L:2272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65 after pos.:60
M:341 Repeated in SeqNo=65
L:2318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66 after pos.:16
L:2715 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71 after pos.:60
M:341 Repeated in SeqNo=71
L:2760 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72 after pos.:16
L:3078 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:300
M:341 Repeated in SeqNo=79
L:3115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80 after pos.:96
M:341 Repeated in SeqNo=80
L:3260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84 after pos.:112
L:3425 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90 after pos.:16
M:341 Repeated in SeqNo=90
L:3584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97 after pos.:60
L:3601 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:98
L:3978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109 after pos.:0
M:341 Repeated in SeqNo=109
L:4117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110 after pos.:0
M:341 Repeated in SeqNo=110
L:4332 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:115
L:4341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115 after pos.:240
L:4371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116 after pos.:80
L:4758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:124 after pos.:32
M:341 Repeated in SeqNo=124
L:5035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:130 after pos.:64
L:5496 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:143
L:5503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:143 after pos.:120
M:341 Repeated in SeqNo=143
L:5529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:144 after pos.:32
M:341 Repeated in SeqNo=144
L:5597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:146 after pos.:64
L:5746 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:149

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```
L:5768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:149 after pos.:1020
L:5848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:150 after pos.:256
M:341 Repeated in SeqNo=150
L:6805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:168 after pos.:16
M:341 Repeated in SeqNo=168
L:7233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:184 after pos.:0
L:7385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:190 after pos.:0
L:7626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:196 after pos.:0
L:8143 M:254 E: No. of Bases conflict, LENGTH:Input:240 Counted:239 SEQ:213
L:8143 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
M:254 Repeated in SeqNo=213
L:8146 M:252 E: No. of Seq. differs, <211> LENGTH:Input:393 Found:391 SEQ:213
L:8158 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:214
L:8869 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:232
M:340 Repeated in SeqNo=232
L:8903 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:234
L:9503 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:250
L:9768 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:255
L:9789 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:256
M:340 Repeated in SeqNo=256
L:9994 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:261
L:10013 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:262
M:340 Repeated in SeqNo=262
L:10121 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:264
L:10417 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:274
M:340 Repeated in SeqNo=274
L:10695 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:279
M:340 Repeated in SeqNo=279
L:10709 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:280
M:340 Repeated in SeqNo=280
L:10988 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:285
M:340 Repeated in SeqNo=285
L:11081 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:286
L:11269 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:292
M:340 Repeated in SeqNo=292
L:11391 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:296
M:340 Repeated in SeqNo=296
L:11439 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:298
L:11484 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:300
L:12272 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:318
M:340 Repeated in SeqNo=318
L:12374 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:320
L:12613 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:330
L:12749 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:336
L:12795 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:338
L:12966 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:342
L:14041 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:361
M:340 Repeated in SeqNo=361
L:14073 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:362
```

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```
M:340 Repeated in SeqNo=362
L:14281 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:366
M:340 Repeated in SeqNo=366
L:14510 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:371
L:14557 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:372
L:14755 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:378
L:15181 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:393
M:340 Repeated in SeqNo=393
L:15255 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:396
M:340 Repeated in SeqNo=396
L:15795 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:408
M:340 Repeated in SeqNo=408
L:76811 M:252 E: No. of Seq. differs, <211> LENGTH:Input:770 Found:722 SEQ:1818
```